

SEQUENCE LISTINGS

| SEQ ID NO | CLONE NAME | SEQUENCE |
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| SEQ ID NO: 1 | 405 (pumilus) | <pre> ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGGTGCTGTCAGTCACATCGC TGTTGCGATGCAGCCGTAGCAAAAGCCGCT GAACACAATCCAGTTGTTATGGTCACGGTAT CGGAGGAGCTTCATACAATTTCGCGGAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCACGG GGCAAGCTGTATGCGGTTGATTTGGACAA GACAGGGACGAATTATAACAATGGCCCGGTAT TATCACGATTGTGCAAAAGGTTTAGACGAA ACGGGTGCGAAAAAGTGGATATTGTCGCTCA CAGTATGGTGGCGCGAACACACCTTACTACA TAAAAAACTGGACGGCGGAAATAAAATTGAA AACGTCGTAACGCTTGGCGCGCGAACCGTTC GACGACAAGCAAGCGCTTCCGGGAACAGATC CAAATCAAAGATTTATACACATCCATTAC AGCAGTGCCGATATGATTGTCATGAATTACTT ATCAAAATTAGACGGTGCTAAAACGCTCAA TTCATGGCGTTGGGCACATTGGTTATTGATG AACAGCCAAGTCAACAGCCTGATTAAAGAAGG ACTGAACGGCGGGGGCAAAATAACGAATTAA </pre> |
| SEQ ID NO: 2 | 406 (subtilis) | <pre> ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGATGCTGTCAGTCACATCGC TGTTGCGTTGCAGCCGTAGCAAAAGCCGCT GAACACAATCCAGTCGTTATGGTCACGGTAT TGGAGGGGCATTCATTCAATTTCGCGGAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCGCGG GACAAGCTGTATGAGTTGATTTGGACAA GACAGGCACAAATTATAACAATGGACCGGTAT TACCAACGATTGTGCAAAAGGTTTAGATGAA ACGGGTGCGAAAAAGTGGATATTGTCGCTCA CAGCATGGGGGGCGCGAACACACTTACTACA TAAAAAACTGGACGGCGGAAATAAGTTGCA AACGTCGTAACGCTTGGCGCGAACCGTTC GACGACAGGCAAGCGCTTCCGGGAACAGATC CAAATCAAAGATTTATACACATCCATTAC AGCAGTGCCGATATGATTGTCATAAATTACTT ATCAAGATTAGATGGTGCTAGAACGTTCAA TCCATGGCGTTGGACACATCGGCCTCTGTAC AGCAGCCAAGTCAACAGCCTGATTAAAGAAGG GCTGAACGGCGGGGGACTCAATACAAATTAG </pre> |
| SEQ ID NO: 3 | 402 (megaterium) | <pre> ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGGTGCTGTCAGTCACATCGC TGTTGCGATGCAGCCGTAGCAAAAGCCGCT GACACAATCCAGTTGTTATGGTCACGGTAT </pre> |

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| | | CGGAGGAGCTTCATACAATTTCGGGAATTA AGAGCTATCTGTATCTCAGGGCTGGTCACGG GGCAAGCTGTATGCAGGGTGTGATTTGGGACAA GACAGGGACGAATTATAACAATGGCCCGGTAT TATCAGCAGTTGTGCAAAAGGTTAGACGAA ACGGGTGCGAAAAAGTGGATATTGTCGCTCA CAGCATGGGTGGCGCGAACACACTTACTACA TAAAAAAATCTGGACGGCGGAAATAAAATTGAA AACGTCGTAACGCTTGGCGCGCGAACCGTT GACGACAAGCAAGGCCTCCGGGAACAGATC CAAATCAAAGATTATACACATCCATTAC AGCAGTGCCGATATGATTGTCATGAATTACTT ATCAAAATTAGACGGTGCTAAAACGTTCAA TTCATGGCAGGGCAGGGTATTGTTATTGATG AACAGCCAAGTCAACAGCCTGATTAAAGAAGG ACTGAACGGCGGGACTAAATACAAATTAA |
| SEQ ID NO: 4 | 400 (lentus) | ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAAACAATTGGTGTGTCAGTCACATCGC TGTGGCGATGCAGCCGTACGAAAAGCCGCT GAACACAATCCAGTTGTTATGGTTACGGTAT CGGAGGAGCTTCATACAATTTCGGGAATTA AGAGCTATCTGTATCTCAGGGCTGGTCACGG GGCAAGCTGTATGCAGGGTGTGATTTGGGACAA GACAGGGACGAATTATAACAATGGCCCGGTAT TATCAGCAGTTGTGCAAAAGGTTAGACGAA ACGGGTGCGAAAAAGTGGATATTGTCGCTCA CAGCATGGGTGGCGCGAACACACTTACTACA TAAAAAAATCTGGACGGCGGAAATAAAATTGAA AACGTCGTAACGCTTGGCGCGCGAACCGTT GACGACAAGCAAGGCCTCCGGGAACAGATC CAAATCAAAGATTATACACATCCATTAC AGCAGTGCCGATATGATTGTCATGAATTACTT ATCAAAATTAGACGGTGCTAAAACGTTCAA TTCATGGCAGGGCAGGGTATTGTTATTGATG AACAGCCAAGTCAACAGCCTGATTAAAGAAGG ACTGAACGGCGGGACTAAATACAAATTAA |
| SEQ ID NO: 5 | 396 (circulans) | ATGAAATTATAAAAAGAAGGATCATTGCACT TGTAAACAATTGGTGTGTCAGTCACATCGC TGTGGCGATGCAGCCGTACGAAAAGCCGCT GAACACAATCCAGTTGTTATGGTTACGGTAT CGGAGGAGCTTCATACAATTTCGGGAATTA AGAGCTATCTGTATCTCAGGGCTGGTCACGG GGCAAGCTGTATGCAGGGTGTGATTTGGGACAA GACAGGGACGAATTATAACAATGGCCCGGTAT TATCAGCAGTTGTGCAAAAGGTTAGACGAA ACGGGTGCGAAAAAGTGGATATTGTCGCTCA CAGCATGGGTGGCGCGAACACACTTACTACA |

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| | | TAAAAAAATCTGGACGGCGGAAATAAAATTGAA AACGTCGTAACGCTTGGCGCGCGAACC GTTT GACGACAAGCAAGGCGCTTCCGGGAACAGATC CAAATCAAAGATTTATACACATCCATTAC AGCAGTGCCGATATGATTGT CATGAATTACTT ATCAAAATTAGACGGTGCTAAAACGTTCAAA TTCATGGCGTTGGGCACATTGGTTATTGATG AACAGCCAAGTCAACAGCCTGATTAAAGAAGG ACTGAACGGCGGGGCCTCAATACAAATTAA |
| SEQ ID NO: 6 | 392 (azotoformans) | ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAAACAATTTGGTGCTGTCAGTCACATCGC TGTGGCGATGCAGCCGT CAGCAAAAGCCGCT GAACACAATCCAGTTGTTATGGTTACCGGTAT CGGAGGAGCTTCATACAATTTCGCGGGATTAA AGAGCTATCTCGTATCTCAGGGCTGGTCACGG GGCGAGCTGTATGCGGTTGATTGGGACAA GACAGGGACGAATTATAACAATGGCCCGGTAT TATCACGATTGTGCAAAAGGTTTAGACGAA ACGGGTGCGAAAAAAAGTGGATATTGTCGCTCA CAGCATGGGTGGCGCGAACACACTTTACTACA TAAAAAAATCTGGACGGCGGAAATAAAATTGAA AACGTCGTAACGCTTGGCGCGCGAACC GTTT GACGACAAGCAAGGCGCTTCCGGGAACAGATC CAAATCAAAGATTTATACACATCCATTAC AGCAGTGCCAATATGATTGT CATGAATTACTT ATCAAAATTAGACGGTGCTAAAACGTCACAA TTCATGGCGTTGGGCACATTGGTTATTGATG AACAGCCAAGTCAACAGCCTGATTAAAGAAGG ACTGAACGGCGGGGCCTAGATAACAAATTAA |
| SEQ ID NO: 7 | 398 (firmus) | ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAAACAATTTGGTGCTGTCAGTCACATCGC TGTGGCGATGCAGCCGT CAGCAAAAGCCGCT GAACACAATCCAGTTGTTATGGTTACCGGTAT CGGAGGAGCTTCATACAATTTCGCGGGATTAA AGAGCTATCTCGTATCTCAGGGCTGGTCACGG GGCAAGCTGTATGCGGTTGATTGGGACAA GACAGGGACGAATTATAACAATGGCCCGGTAT TATCACGATTGTGCAAAAGGTTTAGACGAA ACGGGTGCGAAAAAAAGTGGATATTGTCGCTCA CAGCATGGGTGGCGCGAACACACTTTACTACA TAAAAAAATCTGGACGGCGGAAATAAAATTGAA AACGTCGTAACGCTTGGCGCGCGAACC GTTT GACGACAAGCAAGGCGCTTCCGGGAACAGATC CAAATCAAAGATTTATACACATCCATTAC AGCAGTGCCGATATGATTGT CATGAATTACTT ATCAAAATTAGACGGTGCTAAAACGCTCAAA TTCATGGCGTTGGGCACATTGGTTATTGATG |

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| | | AACAGCCAAGTCAACAGCCTGATTAAAGAAGG ACTGAACGGCGGAGGCCACAATACAAATTAA |
| SEQ ID NO: 8 | 393 (badius) | ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGGTGCTGTCAGTCACATCGC TGTTTGCATGCAGCCGTCAAGCAAAAGCCGCT GAACACAATCCAGTTGTTATGGTCACGGTAT CGGAGGAGCTTCATACAATTTCGCGGAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCACGG GGCAAGCTGTATCGGGTGATTGGACAA GACAGGGACGAATTATAACAATGGCCCGGTAT TATCACGATTGTGCAAAAGGTTAGACGAA ACGGGTGCGAAAAAGTGGATATTGTCGCTCA CAGCATGGTGGCGCGAACACACTTTACTACA TAAAAAACTGGACGGCGGAAATAAAATTGAA AACGTCGTAACGCTTGGCGCGAACCGTT GACGACAAGCAAGGCCTCCGGGAACAGATC CAAATCAAAGATTATACACATCCATTAC AGCAGTGCCGATATGATTGTCATGAATTACTT ATCAAATTAGACGGTGCTAAAACGTTCAAA TTCATGGCGTTGGGCACATTGGTTATTGATG AACAGCCAAGTCAACAGCCTGATTAAAGAAGG ACTGAACGGCGGAGGCCACAATACAAATTAA |
| SEQ ID NO: 9 | Dc5h | ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGATGCTGTCCTGTTACATCGC TGTTTGCATGCAGCAACCGTCAGCAAAAGCCGCT GAACACAATCCAGTCGTTATGGTCACGGTAT TGGAGGGGCATTCATTCAATTTCGCGGAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCGCG GACAAGCTGTATGCAGTTGATTCAAGGACAA GACAGGCACAAATTATAACAATGGCCCGGTAT TATCACGATTGTGCAAAAGGTTAGATGAA ACGGGTGCGAAAAAGTGGATATTGTCGCTCA CAGCATGGGGGGCGCGAACACACTTTACTACA TAAAAAACTGGACGGCGGAAATAAGTTGAA AACGTCGTAACGCTTGGCGCGAACCGTT GACGACAGGCAAGGCCTCCGGGAACAGATC CAAATCAAAGATTATACACATCCATTAC AGCAGTGCCGATATGATTGTCATGAATTATT ATCAAGATTAGATGGTGCGAGAAACGTTCAAA TCCATGGCGTTGGACACATCGGCCTCTGTAC AGCAGCCAAGTCAACAGCCTGATTAAAGAAGG GCTGAACGGCGGGGGCCTCAATACAAATTAA |
| SEQ ID NO: 10 | Dc5f | ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGATGCTGTCCTGTTACATCGC TGTTTGCATGCAGCAACCGTCAGCAAAAGCCGCT GAACACAATCCAGTCGTTATGGTCACGGTAT TGGAGGGGCATTCATTCAATTTCGCGGAATTA |

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| | | AGAGCTACCTCGTATCTCAGGGCTGGTCGCGG GACAAGCTGTATGCAGTTGATTCTAAGACAA AACAGGGAATAACCGCAACAAATGGTCCCGCGTC TATCGAGATTCTGTCAAAGATGTGTTAGACAAA ACGGGTGCCAAAAAGTAGATATTGTGGCTCA TAGTATGGGTGGAGCGAACACGCTATACTATA TCAAGAATCTAGATGGCGGCATAAAATTGAG AACGTTGTCACAATTGGTGGAGCAAACGGACT CGTTTCAAGCAGAGCATTACCAGGCACAGATC CAAATCAAAAAATTCTTACACATCCGTCTAT AGCTCAGCAGATCTTATTGTCGTCAACAGCCT CTCTCGTTAATTGGCGCAAGAACATCCTGA TCCATGGCGTTGGTCATATCGGTCTATTAACC TCAAGCCAAGTGAAGGGTATATTAAAGAAGG ACTGAACGGCGGAGGCCTCAATACAATTAA |
| SEQ ID NO: 11 | Dc5c1 | ATGAAAGTGATTTTGTAAAGAAAAGGAGTTT GCAAATTCTTGTGCCCCTTGCTTAGTGCTAG GTTCAATAGCCTTCATCCAGCGAAAGAACGC AAAGCGGCTGAGCATAATCCGGTTGTAATGGT GCATGGCATGGGTGGTGCCTTATAACTTTG CTTCGATCAAACGATACTTAGTATCACAGGG TGGGATCAAAACCAACTTTGCAATCGATT CATAGACAAAACAGGCAATAACCTAAACAATG GCCCGAGGCTCTCGAGATTGAAAGACGTA CTAGCCAAAACGGCGCAAAAAAGTAGATAT TGTGGCTCATAGTATGGCGGTGCGAACACGT TATACTATATTAAAAACCTAGACGGTGGAGAT AAAATTGAAAACGTCGTACATTAGGTGGAGC AAACGGACTCGTATCACTCAGAGCATTACAG GCACCGATCCAAATCAAAAATTCTTACACA TCTGTCTATAGCTCAGCCGATCTCATTGTCGT CAACAGCCTTCGCGTTAATTGGCGCAAGAA ACGTCCTGATCCACGGCGTTGGACATATCGGT CTATTAACCTCAAGCCAAGTCAAAGGCTATGT GAAAGAAGGATTGAATGGCGGGGGACAGAATA CAAATTAA |
| SEQ ID NO: 12 | Dc5a2 | ATGAAAGTGATTTTGTAAAGAAAAGGAGTTT GCAAATTCTTGTGCTTGCTTAGGTGATGG GTTCAATGGCCTTCATCCAGCCAAAAGAGATC AGAGCGGCTGAGCATAATCCGGTTGATGGT ACATGGCATGGCGGTGCCTTATAACTTTG CTTCGATTTAAAGTTACTGGTATCACAAGGA TGGGATCGAAACCAATTATTGCTATCGATT CATAGACAAAACAGGTAATAACCGCAACAATG GTCCCGGTCTATCCAGATCGTCAAAGATGTG CTAGCCAAAACAGGTGCCAAAAAGTTGATAT TGTGGCTCATAGTATGGCGGAGCGAACACGT |

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| | | TATACTATATTAAGAATCTAGACGGCGGCAT AAAATAGAAAACGTTGTTACACTTGGTGGAGC GAACGGACTCGTTCACTCAGAGCATTACAG GCACCGATCCAAATCAAAAAATCCTTACACA TCCGTCTACAGCTCAGCCGATCTTATCGTCGT CAACAGCCTCTCGCGTTAATTGGCGCAAGAA ACGTCCCTATTACGGCGTGGTCACATCGGT CTATTAGCTTCAAGCCAAGTCAAAGGCTATAT CAAAGAAGGACTGAATGGCGGAGGCCAAAATA CAAATTAA |
| SEQ ID NO: 13 | Dc512 | ATGAAAGTGATTTGTTAAGAAAAGGAGTTT GCAAATTCTCATTCGCGCTTGCATTGGTGTATTG GTTCAATGGCGTTATCCAGCCGAAAGAGGCG AAGGCGGCTGAGCATAATCCGGTTGTGATGGT GCATGGCATTGGCGGTGCCTCTTATAACTTTT TTTCTATTAAAAGTTATTGGCCACACAAGGC TGGGATCGAAACCAATTATATGCTATTGATT CATAGACAAAACAGGAAATAACCGCAACAATG GTCCCGCGTCTATCGAGATTCTCGTAAAGATGTG TTAGACAAAACGGGTGCCAAAAAGTAGATAT TGTGGCTCATAGTATGGGTGGAGCGAACACGC TATACTATATCAAGAATCTAGATGGCGGCGAT AAAATTGAGAACGTTGTCACAATTGGTGGAGC AAACGGACTCGTTCAAGCAGAGCATTACAG GCACAGATCCAAATCAAAAAATTCTTACACA TCCGTCTATAGCTCAGCAGATCTTATTGTCGT CAACAGCCTCTCTCAGTTAATTGGCGCAAGA AACATCCTGATCCAGGCGTGGTCATATCGGT CTATTAACTCAAGCCAAGTGAAAGGGTATAT TAAAGAAGGACTGAACGGCGGAGGCCCTCAATA CAAATTAA |
| SEQ ID NO: 14 | Sga | ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTGATGCTGTCGTGTTACATCGC TGTTGCGTTGCAACCGTCAGCAAAAGCCGCT GAACACAATCCAGTCGTTATGGTTACCGGTAT TGGAGGGGCATCAATTGCGGGATTAA AGAGCTATCTCGTATCTCAAGGCTGGTCGCGG GACAAGCTGTATGCAGTTGATTTCAGGGACAA GACAGGCAATAACTTAAACAACGGTCCAGTAT TATCGCGTTCTGTGAAAAGGTATTAGATGAA ACCGGTGCGAAAAAGTGGATATTGTCGCTCA CAGCATGGCGGGCCTAACACGCTTACTACA TAAAAAATTGGATGGCGGTAAATAAAATTGAA AACGTCGTAACACTGGCGGCGGAATCGTCT TGTGACAGGCAAGGCGCTTCCGGTACTGATC CCAACCAAAAGATCTTGTACACATCCGTTAC AGTAGTGCTGATATGATTGTTATGAATTACTT |

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| | | AACAAAATTAGACGGGGCTAAAATGTTAAA TTCATGGTGTGGACATATCGGCCTCTGTAC AGCAGCCAAGTCAACAGCCTGATTAAAGAAGG GCTTAACGGCGGAGGCCTCAATACAAATTAA |
| SEQ ID NO: 15 | Sgc | ATGAAATTGTAAAAGAAGGATCATTGCACT TGTAACAATTTGATGCTGTCTGTTACATCGC TGTTTGCCTTGCAACCGTCAGCAAAAGCCGCT GAACACAATCCAGTCGTTATGGTCACGGTAT TGGAGGGGCATCATTCAATTTGCGGAAATTAA AGAGCTATCTCGTATCTCAGGGCTGGTCGCGG GACAAGCTGTATGCAGTTGATTTCTGGGATAAA GACAGGCAATAACTAAACAAACGGTCCAGTAT TATCGCGTTTGTGAAAAAGGTATTAGATGAA ACCGGTGCGAAAAAGTGGATATTGTCGCTCA CAGCATGGCGGCGCTAACACGCTTACTACA TAAAAAAATTGGATGGCGGTAAATAAAATTGAA AACGTCGTAACACTTGGCGCGCGAATCGTCT TGTGACAGGCAAGGCCTCCGGTACTGATC CCAACCAAAAGATATTGTACACATCCGTTAC AGTAGTGCTGATATGATTGTTATGAATTACTT ATCAAAATTAGACGGGGCTAAAATGTTAAA TTCATGGTGTGGACATATCGGCCTCTGTAC AGCAGCCAAGTCAATAGCCTGATTAAAGAAGG GCTTAACGGCGGAGGACTCAATACGAATTAA |
| SEQ ID NO: 16 | Sgd | ATGAAATTGTAAAAGAAGGATCATTGCACT TGTAACAATTTGATGCTGTCTGTTACATCGC TGTTTGCCTTGCAACCGTCAGCAAAAGCCGCT GAACACAATCCAGTCGTTATGGTCACGGTAT TGGAGGGGCATCATTCAATTTGCGGAAATTAA AGAGCTATCTCGTATCTCAGGGCTGGTCGCGG GACAAGCTGTATGCAGTTGATTTAGTGACAA AACAGGCAATAACTAAACAAACGGTCCAGTAT TATCGCGTTTGTGAAAAAGGTATTAGATGAA ACCGGTGCGAAAAAGTGGATATTGTCGCTCA CAGCATGGCGGCGCTAACACGCTTACTACA TAAAAAAATTGGATGGCGGTAAATAAAATTGAA AACGTCGTAACACTTGGCGCGCGAATCGTCT TGTGACAGGCAAGGCCTCCGGTACTGATC CCAACCAAAAGATCTTGTACACATCCGTTAC AGTAGTGCTGATATGATTGTTATGAATTACTT ATCAAAATTAGACGGGGCTAAAATGTTAAA TTCATGGTGTGGACATATCGGCCTCTGTAC AGCAGCCAAGTCAACAGCCTGATTAAAGAAGG GCTTAACGGCGGGGGCCTGAATACGAATTAA |
| SEQ ID NO: 17 | Sgf | ATGAAATTGTAAAAGAAGGATCATTGCACT TGTAACAATTTGATGCTGTCTGTTACATCGC TGTTTGCCTTGCAACCGTCAGCAAAAGCCGCT |

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| | | GAACACAATCCAGTCGTTATGGTTACGGTAT TGGAGGGGCATCATTCAATTTCAGGGCTGGTCGCGG GACAAGCTGTATGCAGTTGATTCAAAGACAA GACAGGGAAATAACCGCAACAATGGTCCGCGTC TATCGAGATTCTGTCAAAGATGTGTTAGACAAA ACAGGGAGCCAAAAAAAGTAGATATTGTGGCTCA TAGTATGGCGGGAGCGAACACATTACTATA TTAAGAATCTAGATGGTGGCGATAAAATTGAG AACGTTGTCACAATTGGTGGAGCAAACGGACT CGTTCAAGCAGAGCATTACCAGGCACAGATC CAAATCAAAAAATTCTTACACATCCGTCTAT AGCTCAGCAGATCTTATTGTCGTCAACAGTCT CTCTCGTTAATTGGCGCAAGAAACGTCCAAA TCCATGGCGTTGGACATATCGGTCTATTAACC TCAAGCCTAGTCAAAGGATATATTAAAGAAGG ACTGAACGGCGGGAGGCCAAAATACAAATTAA |
| SEQ ID NO: 18 | Sgh | ATGAAATTGTAAGAAAGGATCCTTGCAC TGTAACAATTGATGCTGCTGTTACATCGC TGTTGCGTTGCAACCGTCAGCAAAGCCGCT GAACACAATCCAGTCGTTATGGTTACGGTAT TGGAGGGGCATCATTCAATTTCAGGGCTGGTCGCGG GACAAGCTGTATGCAGTTGATTCATTGACAA GACAGGGAAATAACCGCAACAATGGTCCGCGTC TATCGAGATTCTGTCAAAGATGTGTTAGACAAA ACAGGGAGCCAAAAAAAGTAGATATTGTGGCTCA TAGTATGGCGGGAGCGAACACATTACTATA TTAAGAATCTAGATGGTGGCGATAAAATTGAG AACGTTGTCACAATTGGTGGAGCAAACGGACT CGTTCAAGCAGAGCATTACCAGGCACAGATC CAAATCAAAAAATTCTTACACATCCGTCTAT AGCTCAGCAGATCTTATTGTCGTCAACAGTCT CTCTCGTTAATTGGCGCAAGAAACGTCCAAA TCCATGGCGTTGGACATATCGGTCTATTAACC TCAAGCCTAGTCAAAGGATATATTAAAGAAGG ACTGAACGGCGGGAGGCCAAAATACAAATTAA |
| SEQ ID NO: 19 | Mt2b1 | ATGAAAGTGATTGTTAAGAAAAGGAGTT GCAAATTCTGTTGCCCTGCCTTAGTGTAG GTTCAATGCCCTTCATCCAGCCAAAAGAAATC AAAGCAGCTGAGCACAATCCGGTTGTGATGGT ACATGGTATTGGAGGGAGCGTCTTATAACTTG CTTCGATTAAGTTATTGGTTACCAAGGC TGGGATCGAAACCAATTATTGCTATCGATT CATAGACAAAACAGGGAAATAACCGCAACAATG GTCCTCGTTATCTAGATTGTCAAAGATGTG CTAGACAAAACGGGTGCCAAAAAAAGTAGATAT |

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| | | TGTGGCGCATAGTATGGCGGGCGAACACGC TATACTATATTAAGAACATCTAGATGGCGGCGAT AAAATTGAAAACGTCGTCACCATTGGTGGAGC AACGGACTCGTTCACTCAGAGCATTACCAAG GAACAGATCCAATCAAAAAATTCTCTATACA TCTGTCTATAGCTCAGCCGATTTGATTGTCGT CAACAGCCTTCGCGTTAACTGGCGCAAGAA ATGTCCTGATCCACGGCGTTGGCCATATCGGT CTATTAACCTCAAGCCAAGTGAAAGGGTATAT TAAAGAAGGACTGAAACGGCGGGGCCTAAATA CAAATTAA |
| SEQ ID NO: 20 | H2a | ATGAAATTTGAAAAAGAAGGATCATTGCACT TGTAAACAATTTGATGCTGTCTGTTACATCGC TGTGGCGTTGCAACCGTCAGCAAAAGCCGCT GAACACAATCCAGTCGTTATGGTCACGGTAT TGGAGGGCATTCATTCAATTGCGGGAAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCGCGG GACAAGCTGTATGCAGTTGATTTCAGGGACAA GACAGGAAATAACCGCAACAATGGTCCCGCTC TATCTAAATTCTGTCAAAGATGTGTTAGACAAA ACGGGTGCCAAAAAAGTAGATATTGTGGCTCA TAGTATGGCGGGCGAACACCGCTATACTATA TTAAGAATCTAGATGGCGGCATAAAATTGAG AACGTTGTCACAATTGGCGGAGCAAACGGACT CGTTCAAGCAGAGCATTACCAAGGCACAGATC CAAATCAAAAATTCTTACACATCCGTCTAC AAGCTCAGCCGATCTCATTGTCGTCAACAGTC TCTCTCGTTAATTGGCTGCAAGAAACAGTCC AAATCCATGGCGTTGGACATATCGGTCTATTA ACCTCAAGCCAAGTCAAAGGATATTTAAAGA AGGACTGAAACGGCGGGGACTAAATAACAAATT AA |
| SEQ ID NO: 21 | 1f15(G2) | TGAACACAATCCAGTTGTTATGGTTACCGTA TTGGAGGGCATTCATTCAATTGCGGGAAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGGCAAGCTGTATGCAGGGTGATTGGACAA AGACAGGGACGAATTATAACAATGGCCCGGTA TTATCGCGTTTGTGAAAAAGGTATTAGATGA AACGGGTGCAAAAAGTGGATATTGTCGCTC ACAGCATGGCGGCGCTAACACGCTTACTAC ATAAAAATCTGGACGGCGGAAATAAAAGTTGA AAACGTCGTAACGCTTGGCGGACGAACCGTT CGACGACAAGCAAGGCCTCCGGGAACAGAT CCAAATCAAAGATTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCTAAAATGTTCAA ATTGTCATGGCGTTGGGCACATTGGTTATTGAT |

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| | | GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGACTCAATACGAATTGA |
| SEQ ID NO: 22 | 3C12 | TGAACACAATCCAGTTGTTATGGTTACGGTA TTGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCCTGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGT TTATCTAGATTCTGTCAGGATGTGCTAGACAA AACGGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGGGGGCGCGAACACACTTTACTAC ATAAAAAAATCTGGACGGCGGAATAAAATTGA AACGTCGTAACGCTTGGCGCGAACCGTT CGACGACAAGCAAGGCCTCCGGGAACAGAT CCAAATCAAAGATTTTATACACATCCATT CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAATTAGACGGGCTAAAAATGTTCAA ATTCACTGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGACTCAATACGAATTGA |
| SEQ ID NO: 23 | 3N19(G2) | TGAACACAATCCAGTTGTTATGGTTACGGTA TTGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCCTGTTGATTTGGGACA GGACAGGGACGAATTATAACAATGGCCCGGT TTATCACGATTGTGAAAAAGTATTAGATGA AACCGGTGCGAAAAAGTGGACATTGTCGCTC ACAGCATGGTGGCGCGAACACACTTTACTAC ATAAAAAAATCTGGACGGCGGAATAAAATTGA AACGTCGTAACGCTTGGCGCGAACCGTT TGACGACAAGCAAGGCCTCCGGGAACAGAT CCAAATCAAAGATTTTATACACATCCATT CGGCAGTGCCGATATGATTGTCATGAATTACT TATCAAATTAGACGGTGCTAAAACGTTCAA ATCCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGACTGAATAAAATTGA |
| SEQ ID NO: 24 | G2.2 | TGAACACAATCCAGTTGTTATGGTTACGGTA TCGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCCTGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGT TTATCACGATTGTGCAAAGGTTTAGACGA AACGGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGGGGGCGCGAACACACTTTACTAC ATAAAAAAATCTGGACGGCGGAATAAAATTGA AACGTCGTAACGCTTGGCGCGAACCGTT CGACGACAAGCAAGGCCTCCGGGAACAGAT |

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| | | CCAAATCAAAAGATTTATACACATCCATT CGGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTACAA ATTCAATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGACTCAATACGAATTGA |
| SEQ ID NO: 25 | 2C3 | TGAACACAATCCAGTTGTTATGGTTACGGTA TTGGAGGGGCATCATTCAATTGCGGGAAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATCGGGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGT TTATCACGATTGCGAAAAGGTTTAGACGA AACGGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGCGGGCGCAACACACTTACTAC ATAAAAATTGGATGGCGTAATAAAATTGA AACACGTCGTACCCATTGGTGGAGCAAACGGAC TCGTTCAAGCAGAGCATTACCAAGGCACAGAT CCAAATCAAAAATTCTTACACATCCGTCTA TAGCTCAGCAGATCTTATTGTCGTCAACAGTC TCTCTCGTTAATTGGCGCAAGAAACGTCCAA ATCCATGGCGTTGGACATATCGGTCTATTAAC CTCAAGCCAAGTCAAAGGATATATTAAAGAAG GGCTTAACGGCGGGGCCACAATACGAATTGA |
| SEQ ID NO: 26 | 2F11 | TGAACACAATCCAGTTGTTATGGTTACGGTA TCGGAGGGAGCTTCATACAATTGCGGGAAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATCGGGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGT TTATCACGATTGCGAAAAGGTTTAGACGA AACCGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGGTGGCGCAACACACTTACTAC ATAAAAATCTGGACGGCGGAAATAAAATTGA AACACGTCGTACCGCTGGCGCGAACCGTT TGACGACAAGCAGGGCGCTCCGGGAACAGAT CCAAATCAAAAGATTATACACATCCATT CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTACAA ATTCAATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAAAGGATATATTAAAGAAG GACTGAACGGCGGAGGCCTAAATACGAATTGA |
| SEQ ID NO: 27 | KV11(6C7) | TGAACACAATCCAGTTGTTATGGTTACGGTA TTGGAGGGGCATCATTCAAGTTGCGGGAAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATCCGGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGT TTATCACGATTGCGAAAAGGTTGGACGA AACGGGTGCGAAAAAGTGGATATTGTCGCTC |

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| | | ACAGTATGGTGGCGAACACACTTACTAC ATAAAAAATCTGGACGGCGAAATAAAATTGA AACGTCGTAACGCTTGGCGCGAACCGTT TGACGACAAGCAAGGCCTCCGGGTACTGAT CCCAACCAAAAGATCTTGTACACATCCGTTA CAGTAGTGTGATATGATTGTTATGAATTACT TATCAAATTAGACGGGCTAAAATGTTCAA ATTCATGGCGTTGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GAUTGAACGGCGGGGGCTAAATACAAATTGA |
| SEQ ID NO: 28 | KV6(3A1) | TGAACACAATCCAGTTGTTATGGTTACGGTA TTGGAGGGCATCATTCAAGTTTGCAGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCAGGGTTGATTTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGTA TTATCACGATTGTGCAAAAGGTTTGGACGA AACGGGTGCGAAAAAAGTGGATATTGTCGCTC ACAGTATGGTGGCGAACACACTTACTAC ATAAAAAATCTGGACGGCGAAATAAAATTGA AACGTCGTAACGCTTGGCGCGAACCGTT TGACGACAAGCAAGGCCTCCGGGAACAGAT CCCAACCAAAAGATCTTGTACACATCCGTTA CAGTAGTGTGATATGATTGTTATGAATTACT TATCAAATTAGACGGGCTAAAATGTTCAA ATTCATGGCGTTGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GAUTGAACGGCGGGGGCTAAATACAAATTGA |
| SEQ ID NO: 29 | KV2(2D1) | TGAACACAATCCAGTTGTTATGGTTACGGTA TCGGAGGGAGCTTCATACAGTTTGCAGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCAGGGTTGATTTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGTA TTATCACGATTGTGCAAAAGGTTTGGACGA AACGGGTGCGAAAAAAGTGGATATTGTCGCTC ACAGCATGGTGGCGAACACACTTACTAC ATAAAAAATCTGGACGGCGAAATAAAATTGA AACGTCGTAACGCTTGGCGCGAACCGTT TGACGACAAGCAAGGCCTCCGGGAACAGAT CCCAACCAAAAGATCTTGTACACATCCGTTA CAGTAGTGTGCGATATGATTGTCATGAATTACT TATCAAATTAGACGGGCTAAAATGTTCAA ATTCATGGTGTGGACATATCGGCCCTCTGTA CAGCAGCCAAGTCAACAGCCTGATTAAAGAAG GAUTGAACGGCGGGGGCTAAATACAAATTGA |
| SEQ ID NO: 30 | N2.5 | TGAACACAATCCAGTTGTTATGGTTACGGTA TCGGAGGGAGCTTCATACAGTTTGCAGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG |

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| | | GGGCAAGCTGTATCGGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGCAAAAGGTTAGACGA AACGGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGGGGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGAAATAAAATTGA AACAGTCGTAACGCTTGGCGCGCGAACCGTT TGACGACAAGCAAGGCCTCCGGGAACGTGAT CCCAACCAAAAGATCTTGTACACATCCGTTA CAGTAGTGTGATATGATTGTATGAATTACT TATCAAAATTAGACGGGCTAAAAATGTTCAA ATTCATGGCGTTGGGCACACTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GAUTGAACGGCGGGGCCACAATACAAATTGA |
| SEQ ID NO: 31 | KV5(2H6) | TGAACACAATCCAGTTGTTATGGTCACGGTA TTGGAGGGAGCATCATAAATTGCGGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATACGGTTGATTTGGGACA AGACAGGCACAAATTATAACAATGGCCCGTA TTATCACGATTGTGCAAAAGGTTAGACGA AACGGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGGTGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGAAATAAAATTGA AACAGTCGTAACGCTTGGCGCGCGAACCGTC TTGTAACAGGCAAGGCCTCCGGGAACAGAT CCCAATCAAAAGATTTGTACGCATCCGTTA CAGCAGTGCCTGATATGATTGTATGAATTACT TATCAAAATTAGACGGGCTAAAAACGTTCAA ATTCATGGCGTTGGGCACACTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GAUTGAACGGCGGGGCCCTGAATACAAATTGA |
| SEQ ID NO: 32 | 3E5 | TGAACACAATCCAGTCGTTATGGTCACGGTA TTGGAGGGGCATCATTCAATTGCGGGAATT AGGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATCGGGTTGATTTGGGACA GGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGCAAAAGGTTAGATGA AACCGGTGCGAAAAAGTGGACATTGTCGCTC ACAGCATGGGTGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGAAATAAAATTGA AACAGTCGTAACGCTTGGCGCGCGAACCGTT TGACGACAAGCAAGGCCTCCGGGAACAGAT CCAAATCAAAAGATTTATACACATCCATTAA CAGCAGTGCCTGATATGATTGTATGAATTACT TATCAAAATTAGACGGGCTAAAAATGTTCAA ATTCCATGGCGTTGGACACATCGGCCTCTGTA CAGCAGCCAAGTCAACAGCCTGATTAAAGAAG |

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| | | GACTGAACGGCGGGGGCTCAATACGAATTGA |
| SEQ ID NO: 33 | G2.1 | TGAACACAATCCAGTTGTTATGGTTACGGTA TCGGAGGGGCATCATTCAATTTCGCGGAATT AGGAGCTATCTCGTATCTCAGGGCTGGTCACG GGCAAGCTGTATCGCGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCAGATTGTGCAAAAGGTTTAGACGA AACCGGTGCGAAAAAAAGTGGACATTGTCGCTC ACAGCATGGCGGGCTAACACGCTTACTAC ATAAAAAAATCTGGACGGCGAAATAAAATTGA AACAGTCGTAACGCTTGGCGGCACGAACCGTT TGACGACAAGCAGGGCGCTCCGGAACAGAT CCAAATCAAAAGATTTATACACATCCATTAA CAGCAGTGCCTGATATGATTGTCATGAATTACT TATCAAAACTAGACGGTGTAAACAGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGGACTCAATACGAATTGA |
| SEQ ID NO: 34 | 3H24(G2) | TGAACACAATCCAGTTGTTATGGTTACGGTA TTGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGACAAGCCGTATCGCGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCAGATTGTGCAAAAGGTTTAGACAA AACGGGTGCGAAAAAAAGTGGATATTGTCGCTC ACAGCATGGGGGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAATAAGTTGA AACAGTCGTAACGCTTGGCGCGAACCGTT TGACGACAAGCAAGGCCTCCGGAACAGAT CCAAATCAAAAGATTTATACACATCCATTAA CAGCAGTGCCTGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGTAAACAGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGGACTCAATACGAATTGA |
| SEQ ID NO: 35 | KV10(4G6) | TGAACACAATCCAGTTGTTATGGTTACGGTA TTGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTGTCTCAGGGCTGGCGCG GGACAAGCTGTATGCAGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCAGATTGTGCAAAAGGTTTAGACGA AACGGGTGCGAAAAAAAGTGGATATTGTCGCTC ACAGCATGGGTGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAATAAGTTGA AACAGTCGTAACACTTGGCGCGCGAACCGTT TTGTAACAGGCAAGGCCTCCGGGAACGTGAT CCCAACCAAAAGATTTATACACATCCATTAA |

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| | | CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTCGGACATATCGGCCTCTGAT GAACAGCCAAGTCAACACAGCCTGATTAAAGAAG GACTGAACGGCGGGGCCACAATACAAATTGA |
| SEQ ID NO: 36 | KV12(6D4) | TGAACACAATCCAGTTGTTATGGTTACGGTA TCGGAGGGGCATCATTCACTTGCAGGGAAATT AGGAGCTATCTCGTATCTCAGGGCTGGCCGCG GGACAAGCTGTATGCAGGGTTGATTGGGACA AGACAGGCACAAATTATAACAATGGCCCGGT TTATCAGGATTGTGCAAAAGGTATTAGATGA AACCAGGTGCGAAAAAGTGGATATTGTCGCC ACAGCATGGGTGGCGCGAACACACTTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAGTTGA AACAGTCGTGACGCTTGGCGGCCAACCGTT TGACGACAGGCAAGGCGCTCCGGGTACTGAT CCCAATCAAAAGATTATACACATCCGTTA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGGCTGATTAAAGAAG GACTGAACGGCGGAGGCCACAATACAAATTGA |
| SEQ ID NO: 37 | N2.2 | TGAACACAATCCAGTTGTTATGGTTACGGTA TCGGAGGGGCATCATTCACTTGCAGGGAAATT AGGAGCTATCTCGTATCTCAGGGCTGGCCGCG GGACAAGCTGTATGCAGGGTTGATTGGGACA AGACAGGCACAAATTATAACAATGGCCCGGT TTATCAGGATTGTGCAAAAGGTATTAGATGA AACCAGGTGCGAAAAAGTGGATATTGTCGCC ACAGCATGGGTGGCGCGAACACACTTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAGTTGA AACAGTCGTGACGCTTGGCGGCCAACCGTT TGACGACAGGCAAGGCGCTCCGGGTACTGAT CCCAATCAAAAGATTATACACATCCGTTA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGGCTGATTAAAGAAG GACTGAACGGCGGAGGCCACAATACAAATTGA |
| SEQ ID NO: 38 | N2.3 | TGAACACAATCCAGTTGTTATGGTTACGGTA TCGGGGGGGCATCATTCACTTGCAGGGAAATT AGGAGCTATCTCGTATCTCAGGGCTGGCCGCG GGACAAGCTGTATGCAGGGTTGATTGGGACA AGACAGGCACAAATTATAACAATGGCCCGGT TTATCAGGATTGTGCAAAAGGTATTAGATGA AACCAGGTGCGAAAAAGTGGATATTGTCGCC ACAGCATGGGTGGCGCGAACACACTTTACTAC |

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| | | ATAAAAAAATCTGGACGGCGGAAATAAGTTGG AAACGTCGTGACGCTTGGCGGCGCCAACCGTT TGACGACAGGCAAGGCGCTTCCGGGTACTGAT CCCAATCAAAGATTATACACATCCGTTA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGGCTGATTAAGAAG GAUTGAACGGCGGAGGCCACAATACAAATTGA |
| SEQ ID NO: 39 | N2.1 | TGAACACAATCCAGTTGTTATGGTTACGGTA TCGGAGGGGCATCATTCAAGTTGCGGGAATT AGGAGCTATCTGTATCCCAGGGCTGGCCGCG GGACAAGCTGTATGCGGTTGATTTTGGGACA AGACAGGCACAAATTATAACAATGGCCCGGT TTATCACGATTGTCAGAAAGGTATTAGATGA AACCGGTGCGAAAAAGTGGATATTGTCGCC ACAGCATGGTGGCGCGAACACACTTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAGTTGA AAACGTCGTGACGCTTGGCGGCGCCAACCGTT TGACGACAGGCAAGGCGCTTCCGGGTACTGAT CCCAATCAAAGATTATACACATCCGTTA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGGCTGATTAAGAAG GAUTGAACGGCGGAGGCCACAATACAAATTGA |
| SEQ ID NO: 40 | KV4(2E12) | TGAACACAATCCAGTTGTTATGGTTACGGTA TTGGAGGGACATCATTCAAGTTGCGGGAATT AAGAGCTATCTGTATCTCAGGGCTGGTCACG GGACAAGCTGTATGCGGTTGATTTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGT TTATCACGATTGTCAGAAAGGTTTAGACGA AACGGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGCGGCGCGAACACGCTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAAATTGA AAACGTCGTGACGCTTGGCGGCGGAACCGTT TGACGACAGGCAAGGCGCTTCCGGGAACAGAT CCAAATCAAAGATTATACACATCCATT CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAGAAG GAUTGAACGGCGGGGCCACAATACAAATTGA |
| SEQ ID NO: 41 | KV9(4C6) | TGAACACAATCCAGTTGTTATGGTTACGGTA TCGGAGGGGCATCATTCAAGTTGCGGGAATT AAGAGCTATCTGTATCTCAGGGCTGGTCGCG GGACAAGCTGTATGCGAGTTGATTTAGTGACA |

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| | | AAACAGGCACGAATTATAACAATGGCCCGGTA TTATCACGATTGTGCAAAAGGTTAGACGA AACGGTGCAAAAAGTGGATATTGTCGCTC ACAGCATGGGGGCGCGAACACACTTACTAC ATAAAAAAATCTGGATGGCGGTAAATAAATTGA AACGTCGTAACACTTGGCGCGCGAACCGTT TGACGACAAGCAAGGCCTCCGGGTACTGAT CCCAACCAAAAGATCTGTACACATCCATTAA CAGCAGTGCGATATGGTTGTATGAATTACT TATCAAAATTAGACGGGCTAAAATGTTCAA ATTCATGGTGTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGCCACAATACGAATTGA |
| SEQ ID NO: 42 | 7D6 | TAAACACAATCCAGTTATGGTTACGGTA TTGGAGGGGCATCATAACATTTGCGGGAAATA AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGACAAGCTGTATGCAGTTGATTAGTGACA AGACAGGGACGAATTATAACAATGGCCCGGTA TTATCACGATTGTGCAAAAGGTTAGACGA AACGGTGCAAAAAGTGGATATTGTCGCTC ACAGCATGGGGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGGTAAATAAATTGA AACGTCGTAACACTTGGCGCGCGAACCGTT TGACGACAAGCAAGGCCTCCGGGAACAGAT CCAAATCAAAAGATTTTACACATCCATTAA CAGCAGTGCGATATGATTGTATGAATTACT TATCAAAACTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGATTAAATACGAATTGA |
| SEQ ID NO: 43 | 3F3 | TGAACACAATCCAGTTATGGTTACGGTA TTGGAGGGGCATCATTCAATTGCGGGAAATT AAGAGCTATCTCGAATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCGGGTGATTGGGACA AGACCGGGACGAATTATAACAATGGCCCGGTA TTATCACGATTGTGCAAAAGGCTTAGACGA AACGGTGCAAAAAGTGGATATTGTCGCTC ACAGCATGGGTGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAATAAAATTGA AACGTCGTAACGCTTGGCGCGCGAACCGTT TGACGACAAGCAAGGCCTCCGGGAACAGAT CCAAATCAAAAGATTTTACACATCCATTAA CAGCAGTGCGATATGATTGTATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTTCAA ATTCCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGAGAATACGAATTGA |

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| SEQ ID NO: 44 | 2D11(G2) | TGAACACAATCCAGTTATGGTCACGGTA TCGGAGGGGCATCATTCAATTTCGGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGCAAGCTGTATCGGTTGATTTGGGACA GGACAGGGACGAATTATAACAATGGCCCGTA TTATCAGGATTGTGAAAAAGGTATTAGATGA AACCGGTGCGAAAAAGTGGATATTGCGCTC ACAGCATGGGGGGCGCGAACACACTTACTAC ATAAAAATCTGGACGGCGAAATAAAATTGA AACGTCGTACACATTGGCGGCGCGAACCGTT CGACGACAAGCAAGGCGCTCCGGGAACAGAT CCAAATCAAAAGATTTATACACATCCATT CAGCAGTGCCTGATATGATTGTATGAATTACT TATCAAAATTAGACGGTGCTAAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GGCTAACGGCGGGGCCACAATACGAATTGA |
| SEQ ID NO: 45 | 3C23(G2) | TGAACACAATCCAGTTATGGTCACGGTA TTGGAGGGGCATCATTCAATTTCGGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGCAAGCTGTATCGGTTGATTTGGGACA GGACAGGGACGAATTATAACAATGGCCCGTA TTATCAGGATTGTGCAAAGGTTAGACGA AACGGGTGCAAAAAGTGGATATTGCGCTC ACAGCATGGGGGGCGCGAACACACTTACTAC ATAAAAATCTGGACGGCGAAATAAAATTGA AACGTCGTACACATTGGCGGCGCGAACCGTT CGACGACAAGCAAGGCGCTCCGGGAACAGAT CCAAATCAAAAGATTTATACACATCCATT CAGCAGTGCCTGATATGATTGTATGAATTACT TATCAAAATTAGACGGTGCTAAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GGCTAACGGCGGGGCCACAATACGAATTGA |
| SEQ ID NO: 46 | G2.3 | TGAACACAATCCAGTCGTTATGGTCACGGTA TTGGAGGGGCATCATTCAATTTCGGGAATA AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGCAAGCTGTATCGGTTGATTTGGGACA GGACAGGGACGAATTATAACAATGGCCCGTA TTATCAGGATTGTGCAAAGGTTAGACGA AACGGGTGCAAAAAGTGGATATTGCGCTC ACAGCATGGGTGGCGCGAACACACTTACTAC ATAAAAATCTGGACGGCGAAATAAAATTGA AACGTCGTAACGCTTGGCGGCGCGAACCGTT CGACGACAAGCAAGGCGCTCCGGGAACAGAT CCAAATCAAAAGATTTATACACATCCATT CAGCAGTGCCTGATATGATTGTATGAATTGCT |

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| | | TATCAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTTATTGAT GAACAGCCAAGTCACAGCCTGATTAAAGAAG GACTGAACGGCGGGGCCAGAATACGAATTGA |
| SEQ ID NO: 47 | 2A3 | TGAACACAATCCAGTTATGGTTACGGTA TTGGAGGGGCATCGTTCAATTGGGGAAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGACAAGCTGTATGCAGTTGATTCAAAGACA AGACAGGGACGAATTATAACAATGGCCCGGTA TTATCAGATTGTGAAAAAGGTATTAGATGA AACGGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGCGGGCTAACACGCTTACTAC ATAAAGAATCTGGACGGCGAAATAAAATTGA AACAGTCGTAACGCTTGGCGGCGAACCGTT CGACGACAAGCAAGGCGCTCCGGGTACTGAT CCCAACCAAAAGATCTTGTACACATCCGTTA CAGTAGTGCATGATATGATTGTTATGAATTACT TATCAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTTATTGAT GAACAGCCAAGTCACAGCCTGATTAAAGAAG GACTGAACGGCGGAGGCCTAAATACAATTGA |
| SEQ ID NO: 48 | 2F4 | TGAACACAATCCAGTTATGGTTACGGTA TTGGAGGGGCATCATTCAATTGGGGAAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGACAAGCTGTATGCAGTTGATTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGTA TTATCAGATTGTGAAAAAGGTATTAGATGA AACCGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGTGGCGCTAACACGCTTACTAC ATAAAATCTGGACGGCGCGATAAAATTGA AACAGTCGTAACACTTGGCGGCGAACCGTT CGACGACAAGCAAGGCGCTCCGGGAACAGAT CCAAATCAAAGATCTTGTACACATCCGTTA CAGTAGTGCATGATATGATTGTCATGAATTACT TATCAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTTATTGAT GAACAGCCAAGTCACAGCCTGATTAAAGAAG GGCTGAACGGCGGAGGCAGAATACGAATTGA |
| SEQ ID NO: 49 | 2B9(G2) | TGAACACAATCCAGTTATGGTTACGGTA TTGGAGGGGCATCATTCAATTGGGGAAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGACAAGCTGTATGCAGTTGATTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGTA TTATCGCGTTTGTGAAAAAGGTATTAGATGA AACGGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGGGCGCGAACACACTTACTAC ATAAAATCTGGACGGCGAACAAATTGA |

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| | | AAACGTCGTAACACTTGGCGCGCGAACCGTT CGACGACAAGCAAGGCGCTCCGGGAACAGAT CCAAATCAAAGATTATACACATCCATTACAGCAGTGCCGATATGATTGTATGAATTACT TATCAAATTAGACGGGCTAAAAATGTTCAA ATTATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACACAGCCTGATTAAAGAAG GACTGAACGGCGGAGGCCAAAATACGAATTGA |
| SEQ ID NO: 50 | 2C5 | TGAACACAATCCAGTTGTTATGGTTACGGTA TTGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCAGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGTAT TATCGCGTTTGTGAAAAAGGTATTAGATGA AACGGGTGCGAAAAAAAGTGGATATTGTCGCTC ACAGCATGGCGGGCGCTAACACGCTTACTAC ATAAAAAAATCTGGATGGCGGTAAATAAAATTGA AAACGTCGTACACTTGGCGGCGCGAACCGTT CGACGACAAGCAAGGCGCTCCGGGAACGTGAT CCCAACCAAAAGATTATACACATCCATTACAGCAGTGCCGATATGATTGTATGAATTACT TATCAAATTAGACGGTGTAAAAACGTTCAA ATTATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACACAGCCTGATTAAAGAAG GACTGAACGGCGGAGGCCAAAATACGAATTGA |
| SEQ ID NO: 51 | KV1(2A6) | TGAACACAATCCAGTTGTTATGGTTACGGTA TTGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCAGTTGATTTCAAGGACA AGACAGGGACAAATTATAACAATGGCCCGGTAT TATCAGCAGTTGTGAAAAAGGTATTAGATGA AACGGGTGCGAAAAAAAGTGGATATTGTCGCTC ACAGCATGGCGGGCGCTAACACGCTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAAATTGA AAACGTCGTAAACGCTTGGCGGCGCGAACCGTT CGACGACAAGCAAGGCGCTCCGGGTACTGAT CCCAACCAAAAGATTATACACATCCATTACAGCAGTGCCGATATGATTGTATGAATTACT TATCAAATTAGACGGTGTAAAAACGTTCAA ATTATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACACAGCCTGATTAAAGAAG GGCTTAACGGCGGGGCCAGAATACGAATTGA |
| SEQ ID NO: 52 | 2D13(G2) | TAAACACAATCCAGTTGTTATGGTTACGGTA TTGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGACGAGCTGTATGCAGTTGATTTGGGACG AGACAGGGACGAATTATAACAATGGCCCGGTAA |

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| | | TTATCACGATTGTGCAAAAGGTTAGACGA AACCGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGTGGCGCGAACACACTTACTAC ATAAAAATCTGGACGGCGGAATAAAATTGA AACGTCGTAACGCTTGGCGCGAACCGTT CGACGACAAGCAAGGCGCTTCCGGGTACAGAT CCAAATCAAAGATTTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAATTAGACGGTGCTAAAATGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GGCTGAACGGCGGAGGCCAAAATACGAATTGA |
| SEQ ID NO: 53 | 3C8 | TGAACACAATCCAGTTATGGTTACGGTA TCGGAGGGGCATCATTCAATTGGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGACAAAGCTGTATCGGGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGTAA TTATCACGATTGTGCAAAAGGTTAGACGA AACGGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGTGGCGCGAACACACTTACTAC ATAAAAATCTGGACGGCGGAATAAAAGTTGA AACGTCGTAACACTGGCGCGAACCGTT CGACGACAAGCAAGGCGCTTCCGGGAACAGAT CCAAATCAAAGATTTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGCCAAAATACAAATTGA |
| SEQ ID NO: 54 | 2D5 | TGAACACAATCCAGTTATGGTTACGGTA TCGGAGGGGCATCATTCAATTGGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATCGGGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGTAA TTATCACGATTGTGCAAAAGGTTAGACGA AACGGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGTGGCGCGAACACACTTACTAC ATAAAAATCTGGACGGCGGAATAAAATTGA AACGTCGTAACACTGGCGCGAACCGTT CGACGACAAGCAAGGCGCTTCCGGGAACAGAT CCAAATCAAAGATTTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAATTAGACGGTGCTAAAATGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GGCTGAACGGCGGAGGCCAAAATACAAATTGA |

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| SEQ ID NO: 55 | 405 (pumilus) | MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSPRFVQKVLDE TGAKKVDIVAHSMGGANTPYYIKNLDGGNKIE NVVTLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNAQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN |
| SEQ ID NO: 56 | 406 (subtilis) | MKFVKRRIIALVTILVLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFWDKTGTNYNNGPVLPRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVA NVVTLGGANRLTTGKALPGTDPNQKILYTSIY SSADMIVINYLSRLDGARNVQIHGVGHIGLLY SSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 57 | 402 (megaterium) | MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA DTIQLLWFTGIGGASYNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSPRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGHNTN |
| SEQ ID NO: 58 | 400 (lentus) | MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSPRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 59 | 396 (circulans) | MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSPRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 60 | 392 (azotoformans) | MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GELYAVDFWDKTGTNYNNGPVLSPRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSANMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLDTN |
| SEQ ID NO: 61 | 398 (firmus) | MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSPRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY |

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| | | SSADMIVMNYLSKLDGAKNAQIHGVGHIGLLM NSQVNSLIKEGLNGGGHNTN |
| SEQ ID NO: 62 | 393 (badius) | MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSPRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGHNTN |
| SEQ ID NO: 63 | Dc5h | MKFVKRRIIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFKDGTGTNYNNGPVLSPRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVE NVVTLGGANRLTTGKALPGTDPNQKILYTSIY SSADMIVMNYLSRLDGARNVQIHGVGHIGLLY SSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 64 | Dc5f | MKFVKRRIIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFXDKTGNNRNNGPRLSPRFVKDVLDK TGAKKVDIVAHSMGGANTLYYIKNLDGGDKIE NVVTIGGANGLVSSRALPGTDPNQKILYTSVY SSADLIVVNSLSRLIGARNILIHGVGHIGLLT SSQVKGYIKEGLNGGGLNTN |
| SEQ ID NO: 65 | Dc5c1 | MKVIFVKKRSLQILVALALVLGSIAFIQPKEA KAAEHNPPVVMVHGMMGGASYNFASIKRYLVSQG WDQNQLFAIDFIDKTGNNLNNGPRLSPRFVKDV LAKTGAKKVDIVAHSMGGANTLYYIKNLDGGD KIEVVTLGGANGLVSLRALPGTDPNQKILY SVYSSADLIVVNSLSRLIGARNVLIHGVGHI LLTSSQVKGYIKEGLNGGGQNTN |
| SEQ ID NO: 66 | Dc5a2 | MKVIFVKKRSLQILVVLALVMGSMAFIQPKEI RAAEHNPPVVMVHGMMGGASYNFASIKSYLVSQG WDRNQLFAIDFIDKTGNNRNNGPRLSPRFVKDV LAKTGAKKVDIVAHSMGGANTLYYIKNLDGGD KIEVVTLGGANGLVSLRALPGTDPNQKILY SVYSSADLIVVNSLSRLIGARNVLIHGVGHI LLASSQVKGYIKEGLNGGGQNTN |
| SEQ ID NO: 67 | Dc512 | MKVIFVKKRSLQILIALALVIGSMAFIQPKEA KAAEHNPPVVMVHGIGGASYNFFSIKSYLATQG WDRNQLYAIDFIDKTGNNRNNGPRLSPRFVKDV LDKTGAKKVDIVAHSMGGANTLYYIKNLDGGD KIEVVVTIGGANGLVSSRALPGTDPNQKILY SVYSSADLIVVNSLSQFNWRKKHPDPGVGHIG LLTSSQVKGYIKEGLNGGGLNTN |
| SEQ ID NO: 68 | Sga | MKFVKRRIIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFRDKTGNNLNNGPVLSPRFVKKVLDE |

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| | | TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLVTGKALPGTDPNQKILYTSVY SSADMIVMNYLTLDGAKNVQIHGVGHIGLLY SSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 69 | Sgc | MKFVKRRIIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFWDKTGNLNNGPVLRSRFFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLVTGKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLY SSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 70 | Sgd | MKFVKRRIIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFSDKTGNLNNGPVLRSRFFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLVTGKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLY SSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 71 | Sgf | MKFVKRRIIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFDKTGNNRNNGPRLSRFVKDVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGDKIE NVVTIGGANGLVSSRALPGTDPNQKILYTSVY SSADLIVVNSLSRLIGARNVQIHGVGHIGLLT SSQVKGYIKEGLNGGGLNTN |
| SEQ ID NO: 72 | Sgh | MKFVKRRIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFIDKTGNNRNNGPRLSRFVKDVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGDKIE NVVTIGGANGLVSSRALPGTDPNQKILYTSVY SSADLIVVNSLSRLIGARNVQIHGVGHIGLLT SSLVKGYIKEGLNGGGQNTN |
| SEQ ID NO: 73 | Mt2b1 | MKVIFVKRSLQILVALALVIGSMIFIOPKEI KAAEHNPVVMVHGIGGASNFASIKSYLVNQG WDRNQLFAIDFIDKTGNNRNNGPRLSRFVKDVL LDKTGAKKVDIVAHSMGGANTLYYIKNLDGGD KIEENVVTIGGANGLVSLRALPGTDPNQKILY SVYSSADLIVVNSLSRLTGARNVLIHGVGHIG LLTSSQVKGYIKEGLNGGGLNTN |
| SEQ ID NO: 74 | H2a | MKFVKRRIIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFRDKTGNNRNNGPRLSKFVKDVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGDKIE NVVTIGGANGLVSSRALPGTDPNQKILYTSVY KLSRSHCRQQSLSFNWLQETVQIHGVGHIGLL TSSQVKGYIKEGLNGGGLNTN |

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| SEQ ID NO: 75 | 1f15(G2) | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVE NVVTLLGGTNRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 76 | 3C12 | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSRFVVDVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 77 | 3N19(G2) | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDRTGTNYNNGPVLSRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRLLTTSKALPGTDPNQKILYTSIY GSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 78 | G2.2 | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY GSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 79 | 2C3 | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTIGGANGLVSSRALPGTDPNQKILYTSVY SSADLIVVNSLSRLIGARNQIHGVGHIGLLT SSQVKGYIKEGLNGGGHNTN |
| SEQ ID NO: 80 | 2F11 | EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRLLTTSRALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVKGYIKEGLNGGGLNTN |
| SEQ ID NO: 81 | KV11(6C7) | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYPVDFWDKTGTNYNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRLLTTSKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 82 | KV6(3A1) | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRLLTTSKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM |

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| | | NSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 83 | KV2(2D1) | EHNPVVMVHGIGGASYSFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLY NSQVNSLIKEGLNGGGQNTN |
| SEQ ID NO: 84 | N2.5 | EHNPVVMVHGIGGASYSFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGHNTN |
| SEQ ID NO: 85 | KV5(2H6) | EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GKLYTVDFWDKTGTNYNNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLVTGKALPGTDPNQKILYASVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 86 | 3E5 | EHNPVVMVHGIGGASFNFAGIRSYLVSQGWSR GKLYAVDFWDRTGTNYNNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLY NSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 87 | G2.1 | EHNPVVMVHGIGGASFNFAGIRSYLVSQGWSR GKLYAVDFWDKTGTNYNNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGTNRLTTSRALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 88 | 3H24(G2) | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKPYAVDFWDKTGTNYNNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 89 | KV10(4G6) | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWPR DKLYAVDFWDKTGTNYNNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVE SVVTLGGANRLVTGKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGHNTN |
| SEQ ID NO: 90 | KV12(6D4) | EHNPVVMVHGIGGASFSFAGIRSYLVSQGWPR DKLYAVDFWDKTGTNYNNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVE NVVTLGGANRLTTGKALPGTDPNQKILYTSVY |

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| | | SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNRLIKEGLNGGGHNTN |
| SEQ ID NO: 91 | N2.2 | EHNPVVMVHGIGGASFSFAGIRSYLVSQGWPR DKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDE TGAKKVDIVAYSMGGANTLYYIKNLDGGNKVE NVVTLGGANRLTTGKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNRLIKEGLNGGGHNTN |
| SEQ ID NO: 92 | N2.3 | EHNPVVMVHGIGGASFSFAGIRSYLVSQGWPR DKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVG NVVTLGGANRLTTGKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNRLIKEGLNGGGHNTN |
| SEQ ID NO: 93 | N2.1 | EHNPVVMVHGIGGASFSFAGIRSYLVSQGWPR DKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVE NVVTLGGANRLTTGKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNRLIKEGLNGGGHNTN |
| SEQ ID NO: 94 | KV4(2E12) | EHNPVVMVHGIGGTSFN FAGIKSYLVSQGWSR DKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNLSIKEGLNGGGHNTN |
| SEQ ID NO: 95 | KV9(4C6) | EHNPVVMVHGIGGASFSFAGIKSYLVSQGWSR DKLYAVDFSDKTGTNYNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNLSIKEGLNGGGHNTN |
| SEQ ID NO: 96 | 7D6 | KHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR DKLYAVDFSDKTGTNYNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNLSIKEGLNGGGLNTN |
| SEQ ID NO: 97 | 3F3 | EHNPVVMVHGIGGASFN FAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSRFVQKALDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNLSIKEGLNGGGQNTN |
| SEQ ID NO: 98 | 2D11(G2) | EHNPVVMVHGIGGASFN FAGIKSYLVSQGWSR GKLYAVDFWDRTGTNYNNGPVLSRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE |

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| | | NVVTLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN |
| SEQ ID NO: 99 | 3C23(G2) | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDRTGTNYNNGPVLSPRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGHNTN |
| SEQ ID NO: 100 | G2.3 | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDRTGTNYNNGPVLSPRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN |
| SEQ ID NO: 101 | 2A3 | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFKDGTGTNYNNGPVLSPRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN |
| SEQ ID NO: 102 | 2F4 | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFWDKTGTNYNNGPVLSPRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGDKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN |
| SEQ ID NO: 103 | 2B9(G2) | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFWGKTGTNYNNGPVLSPRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN |
| SEQ ID NO: 104 | 2C5 | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSPRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN |
| SEQ ID NO: 105 | KV1(2A6) | EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFKDGTGTNYNNGPVLSPRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN |
| SEQ ID NO: 106 | 2D13(G2) | KHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DELYAVDFWDETGTNYNNGPVLSPRFVQKVLDE |

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| | | TGAKKVDIVAHSMGGANTLYYIKNLGGGNKIE NVVTLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN |
| SEQ ID NO: 107 | 3C8 | EHNPVVMVHGIGGASFNAGIKSYLVSQGWSR DKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLGGGNKVE NVVTLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN |
| SEQ ID NO: 108 | 2D5 | EHNPVVMVHGIGGASFNAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLGGGNKIE NVVTLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN |